Impact of AIP and inhibitory G protein alpha 2 proteins on clinical features of sporadic GH-secreting pituitary adenomas

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Abstract

Introduction: In sporadic acromegaly, downregulation of AIP protein of the adenomas associates with invasive tumor features and reduced responsiveness to somatostatin analogues. AIP is a regulator of Ga_i signaling, but it is not known how the biological function of the Ga_i pathway is controlled.

Aim: To study GNAS and AIP mutation status, AIP and Ga_i-2 protein expressions, Ki-67 proliferation indices and clinical parameters in patients having primary surgery because of acromegaly at a single center between years 2000 and 2010.

Results: Sixty patients (F/M, 31/29), mean age 49 (median 50), mean follow-up 7.7 years (range 0.6–14.0) underwent primary surgery. Four adenoma specimens (6.8%) harbored an AIP and 21 (35.6%) an activating GNAS (Gsp+) mutation. Altogether 13/56 (23%) adenomas had low AIP protein levels, and 14/56 (25%) low Ga_i-2 staining. In regression modeling, AIP expression associated with Ga_i-2 (P = 2.33 × 10⁻⁹) and lower Ki-67 (P = 0.04). In pairwise comparison, low AIP protein predicted high GH at last follow-up (mean 7.7 years after surgery, q = 0.045). Extent of treatments given for acromegaly associated with higher preoperative GH (P = 7.94 × 10⁻⁴), KNOSP (P = 0.003) and preoperative hypopituitarism (P = 0.03) and remission at last follow-up with change in 3-month postoperative IGF1 (P = 2.07 × 10⁻⁷).

Conclusions: We demonstrate, for the first time, that AIP protein expression associates with Ga_i protein intensities in sporadic somatotropinomas, suggesting a joint regulation on somatostatin signaling. Low AIP level associates with higher proliferative activity and predicts high GH concentrations after long-term follow-up. The AIP mutation rate of 6.8% is fairly high, reflecting the genetic composition of the Finnish population.

Introduction

Pituitary adenomas occur with an overall rate of one case in 1064 of the general population (1). Regardless of their benign nature, pituitary adenomas can cause severe health problems related to mass compression, hypopituitarism as well as hormonal hypersecretion.

The majority of pituitary adenomas arise in a sporadic setting and often the exact mechanisms of tumorigenesis remain unknown. Recent next-generation sequencing studies have shown that the somatic landscape of pituitary tumors is relatively silent (2, 3). The primary somatic pathogenic alteration occurring in somatotropinomas is the stimulatory guanine nucleotide (GTP)-binding protein alpha (GNAS) mutation. The GNAS gene (Gsp oncogene) is mutated in approximately 35% of sporadic...
somatotropinomas leading to constitutive activation of cyclic adenosine monophosphate (cAMP) synthesis (4).

Approximately 5% of pituitary tumors occur in the context of hereditary tumor predisposition (5, 6). Germline mutations in the aryl hydrocarbon receptor-interacting protein (AIP) gene predispose to pituitary adenomas (7). AIP mutations are especially enriched in patients with positive family history of homogeneous somatotropinomas and/or a young age at onset, although a subset of patients display neither of these features (5).

Recently, it was discovered that AIP deficiency is associated with pituitary tumorigenesis through elevated intracellular cAMP levels (8, 9). In AIP-deficient cells, constitutive activation of cAMP production was caused by defective inhibitory Ga protein (Ga\(_i\)) signaling and Ga\(_{i-2}\) protein levels were markedly reduced in AIP-associated somatotropinomas (9). The Ga\(_i\) signaling pathway participates in the regulation of somatostatin by inhibiting growth hormone (GH) and prolactin (PRL) secretion and cAMP synthesis through somatostatin receptors (SSTR1–5) (10, 11). The results indicate that AIP acts as a regulator of Ga\(_i\) signaling, but it is not known how AIP controls the proper biological function of the Ga\(_i\) pathway.

Recent studies have indicated that downregulation of AIP protein contributes to the pathogenesis of sporadic pituitary adenomas, regardless of AIP mutation status. In patients with acromegaly, downregulation of AIP appears to predict tumor invasiveness and reduced response to postoperative somatostatin analogue (SSA) treatment. Moreover, it has been shown that preoperative SSA treatment upregulates AIP protein levels, further supporting the role of AIP in SSA signaling (12, 13, 14, 15).

To gain insight into the possible contribution of AIP and Ga\(_{i-2}\) protein expressions on therapeutic outcomes, we studied all consecutive patients with acromegaly (n=60) who underwent primary surgery at the Helsinki University Hospital (HUH) between years 2000 and 2010. We performed AIP and Ga\(_{i-2}\) immunohistochemical (IHC) semiquantitative analyses from the adenoma specimens, and related protein intensities to clinical data and treatment outcomes. We assessed the prevalence of AIP mutations and evaluated the possible influence of somatic GNAS mutation status on these variables.

Subjects and methods

Patient material

The patient cohort comprised 60 patients with acromegaly, who were operated on between years 2000 and 2010 at HUH (16, 17). Of the patients, 29 were males and 31 females with a mean age at surgery of 49 years (median 50). We retrospectively studied the corresponding 60 formalin-fixed paraffin-embedded (FFPE) pituitary adenoma samples (56 GH and 4 GH/PRL) from these patients. Clinical data were collected before and at 3, 6 and 12 months after surgery until the last follow-up. Mean follow-up time after surgery was 7.7 years (range 0.6–14.0). Most of the patients were primarily operated on; five patients received preoperative SSA treatment. All patients underwent pituitary magnetic resonance imaging (MRI) before surgery and at 3 months after surgery, after which follow-up imaging was scheduled on an individual basis.

Biochemical analysis

GH, prolactin (PRL) and insulin-like growth factor 1 (IGF1) measurements were obtained for each patient. Laboratory measurements were performed at HUSLAB, the laboratory of HUH, using standard accredited assays. Serum GH was determined with immunometric TR-IFMA and IGF1 with immunoenzymometric ELISA. IGF1 concentrations were expressed as percentage of upper limit of normal (%ULN). Serum prolactin was determined with immunometric TR-IFMA.

Hormonal remission and hypopituitarism

Biochemical control was defined according to the recent consensus recommendation of 2014 as basal serum GH concentrations <1.0 μg/L and normal age- and gender-standardized serum IGF1 concentrations, and for patients not on SSA treatment as suppression of serum GH concentration <0.4 μg/L on a two-hour oral glucose tolerance test (OGTT) (18). Hypopituitarism was assessed as previously described (17).

Data on the extent of given treatments were collected as an estimate of the aggressiveness of the disease. Different treatment combinations were grouped as follows: (1) patients treated with primary surgery only, (2) patients primarily operated on, treated with adjuvant medical therapy or fractionated stereotactic radiotherapy as well as adjuvant medical treatment or patients who were operated on twice. Group 2 included the tumors most resistant to treatment.

In addition, the treatment response and remission status were assessed by dividing IGF1 response into three groups as done previously (14): group 1, controlled
(IGF1 normalization for age and gender), group 2, partially controlled (non-normalized IGF1 with ≥30% reduction compared to pretreatment values) and group 3, uncontrolled (≤30% decrease in IGF1 concentration or increase compared to pretreatment values).

Ethics

The study was approved by the review board of the Helsinki University Hospital.

DNA isolation and genetic screenings

DNA from FFPE tumors was isolated with NucleoSpin FFPE DNA isolation kit (Macherey-Nagel, Düren, Germany). Mutation screening of AIP was performed using PCR primers designed for FFPE-isolated DNA (Supplementary Table 1, see section on supplementary data given at the end of this article). All six exons and exon–intron junctions were screened. Gain-of-function mutations of the GNAS gene at codons 201 and 227 (Gsp oncogene) were screened as previously described (19). The DNA fragments were amplified using AmpliTaqGold enzyme (Applied BioSystems) and purified using ExoSAP-IT PCR Purification Kit (USB Corporation, Cleveland, OH, USA). The sequencing reactions were performed utilizing the Big Dye Terminator v.3.1 Kit and ABI3730 Automatic DNA Sequencer (Applied BioSystems).

Immunohistochemistry

Antibodies used were mouse monoclonal antibody against AIP (clone35-2, Novus Biologicals LLC, Littleton, CO, USA; 1:500), Gaα2 (T19, sc-7276, Santa Cruz, 1:70) and Ki-67 (MIB-1, M7240, Dako; 1:200). Anti-mouse/rabbit/rat secondary antibody, Poly-HRP-GAM/R/R (DPVB55HRP, Immunologic, Duiven, Netherlands) and DAB chromogen (Thermo Fisher Scientific) were used for detection. AIP protein expressions were semiquantitatively scored according to intensity (0, negative; 1, weak; 2, moderate; 3, strong) and expression pattern (1, patchy; 2, diffuse) as previously described (19). The final protein scores were calculated by multiplying intensity × expression pattern. Gaα2 immunoreaction was scored in a similar way to AIP. Ki-67 scores were obtained by calculating the average percentage of stained nucleus among the cell population. Images were acquired with Leica DM LB microscope (Meyer Instruments, Houston, TX, USA), Olympus DPS0 camera (Olympus Corporation) and Studio Lite software (Licor, Lincoln, NE, USA).

Statistical analyses

Statistical analysis was performed using R (version 3.0.2) and Python (version 2.7, packages NumPy, SciPy and StatsModels).

AIP and Gaα2 levels were categorized into two groups according to the semiquantitative scoring (0–3: low; 4–6: high). Association of both AIP and Gaα2 to a number of clinical variables was tested using the Mann–Whitney U test (SciPy function mannwhitneyu) similar to (14). Both nominal P values and the false discovery rate (FDR) adjusted P values (q-values) corrected with the Benjamins–Hochberg method were calculated.

In addition to pairwise tests, we performed linear regression modeling to account for the dependencies between clinical and genetic variables. A separate linear regression model was constructed to model AIP and Gaα2 protein levels, as well as the extent of treatments, remission status and the change in pre- and post-treatment IGF1 concentrations (ΔIGF1, %ULN). An iterative procedure was used to find a linear model best predicting each of these variables, given clinical and genetic data. The set of explanatory variables considered for each model is described in Supplementary Table 2.

In each of the iterations, the explanatory variable that yielded the highest increase in the R2 adjusted for the number of model variables was added to the model. This procedure was initiated with a model containing no variables. To avoid overfitting while explaining as much variance in data as possible, the model with the lowest Bayesian information criterion (BIC) value was selected as the final model.

Results

AIP and GNAS mutations and clinical characteristics of the patient cohort

All 60 FFPE tumors were successfully sequenced and analyzed for AIP and GNAS mutations. An AIP mutation was identified in four tumors (4/59, 6.8%). A Finnish founder mutation, c.40C>T (Q14X), was found in three tumors and, in one tumor, a short out-of-frame deletion of the patient cohort. All six exons and exon–intron junctions were amplified using AmpliTaqGold enzyme (Applied BioSystems) and purified using ExoSAP-IT PCR Purification Kit (USB Corporation, Cleveland, OH, USA). The sequencing reactions were performed utilizing the Big Dye Terminator v.3.1 Kit and ABI3730 Automatic DNA Sequencer (Applied BioSystems).

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Clinical Study

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AIP and Ga\textsubscript{i-2} in sporadic somatotropinomas

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c.1025C\textgreater A (R201S) and c.1026G\textgreater A (R201H) mutations were both identified once. Exon 9 mutations, c.1104A\textgreater G (Q227R) and c.1104A\textgreater T (Q227L), were detected in one tumor each (ENST00000371085). AIP and GNAS mutations were mutually exclusive.

Characteristics of the 60 patients, grouped according to GNAS mutation positivity (Gsp\textsuperscript{+}, n = 21), wild-type (n = 35) or AIP mutation positivity (AIPmut\textsuperscript{+}, n = 4) are given in Table 1. AIPmut\textsuperscript{+} patients tended to be younger at diagnosis (31 years vs 52 and 49 years for Gsp\textsuperscript{+} and wild-type tumors, respectively), were all characterized by macroadenomas and, in 75% of cases, by a KNOSP grade \textgeq 2 (Table 1). At three months after surgery, 67% (n = 40/58) was in hormonal remission and at last follow-up, after a mean 7.7 (range 0.6–14.0) years 75% (n = 45/58).

Fifty-four patients were operated on once and 6 patients underwent reoperation. Six patients received radiotherapy, and 20 patients received adjuvant medical therapy (SSA in 18 cases, cabergoline in 10 cases and pegvisomant in 3 cases) (Table 1).

Immunohistochemistry

AIP protein immunoreactivity was observed in 55 of 56 AIPmut\textsuperscript{−} tumors (98%). Diffuse cytoplasmic staining was most prominent (Fig. 1B). Occasional nuclear immunoreactivity was also detected. Low AIP expression was observed in 12/56 (21%) of the tumors, one of which stained negative for AIP. Ga\textsubscript{i-2} immunoreaction was positive in all adenomas, with prominent cytoplasmic and membranous staining. Low Ga\textsubscript{i-2} protein expression (intensity \leq 3) was found in 15/56 (27%) adenomas. Tumors with low AIP and Ga\textsubscript{i-2} expression were largely overlapping. Ten tumors with low AIP level (intensity \leq 3) also showed reduced Ga\textsubscript{i-2} expression (Supplementary Fig. 1). Three AIPmut\textsuperscript{+} somatotropinomas with reduced levels (intensity \leq 2).

Figure 1

(A) AIP exon 1 mutations found in sequenced somatotropinomas; a short out-of-the-frame c.70\textless 89delGAGCTCCGGACTTTCAAGA deletion (upper panel) and a Finnish Q14X nonsense mutation (lower panel) with LOH. The upper panel shows the wild-type (WT) and the mutant allele sequences. The deleted region is colored red in the WT sequence. The exact deletion breaking points were confirmed by sequencing the amplicon in both directions. (B) Immunostainings for AIP and Ga\textsubscript{i-2} proteins in somatotropinomas. The upper panel shows diffuse cytoplasmic AIP immunoreactions and the lower panel cytoplasmic/membranous Ga\textsubscript{i-2} stainings in corresponding pituitary tumors. 1 = weak, 2 = moderate and 3 = strong immunoreaction intensity. AIPmut\textsuperscript{+} = AIP mutation-positive somatotropinoma. Scale bar = 10 \textmu m.

c.1025C\textgreater A (R201S) and c.1026G\textgreater A (R201H) mutations were both identified once. Exon 9 mutations, c.1104A\textgreater G (Q227R) and c.1104A\textgreater T (Q227L), were detected in one tumor each (ENST00000371085). AIP and GNAS mutations were mutually exclusive.

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Relationship between AIP and Ga\textsubscript{i-2} protein expression and clinical and hormonal variables

A strong positive association between AIP and Ga\textsubscript{i-2} protein expression levels was observed (Mann–Whitney U test, q = 9.02\times 10^{-5}) (Table 2). AIP expression correlated inversely with last known GH (q = 0.045). These correlations were the only significant pairwise associations to AIP levels with false discovery rate (FDR) <10% (Table 2 and Supplementary Tables 3 and 4). To analyze the relationship of other clinical parameters to AIP levels while controlling for Ga\textsubscript{i-2} levels, linear regression was employed. A regression model consisting of Ga\textsubscript{i-2} expression level, Ki-67 and three-month postoperative GH concentration was constructed, explaining 55% of the variance in AIP levels (R=0.546, P = 6.03\times 10^{-9}).
As expected from the strong pairwise association, most of the variance (43%) was explained by Ga\(_{\text{a},2}\) level only (Ga\(_{\text{a},2}\) regression coefficient \(b=0.678\), 95% CIs (0.492, 0.867), \(P=2.33 \times 10^{-4}\)) (Table 3). In addition, the model was able to identify a weak correlation between higher AIP level and lower Ki-67 proliferation index (\(r=-0.064\), 95% CIs (−0.126, −0.003), \(P=0.04\)). Also, three-month GH concentration improved the strength of the model, although the inverse correlation was not statistically significant (Table 3). An analogous regression model was obtained for Ga\(_{\text{a},2}\), consisting of the AIP level, Ki-67 scores and three-month postoperative GH concentration (\(R^2=0.509\), \(P=3.72 \times 10^{-8}\); Table 4).

The omission of five preoperatively SSA-treated patients from the data did not significantly alter statistical associations or correlations (data not shown).

Predictors of the extent of given treatments and remission status at the end of follow-up

Characteristics of patients treated with surgery only (\(n=37\)) compared to patients receiving any additional treatment (\(n=20\)) are given in Table 5. Patients who needed combined treatments were characterized by higher preoperative GH concentration (\(q=5.63 \times 10^{-4}\)), higher KNOSP grade (\(q=0.045\)) and higher GH (\(q=3.01 \times 10^{-5}\)) and IGF1 (\(q=1.24 \times 10^{-4}\)) concentrations 3 months after surgery (Mann–Whitney U test). Hormonal remission at the end of follow-up was achieved in significantly fewer of the patients needing multimodal treatments compared to those who needed primary surgery only (\(q=0.031\)) (Table 5).

Regression modeling demonstrated that the extent of treatments given for acromegaly associated with more invasive tumor characteristics (\(b=0.432\), 95% CI (0.161, 0.703), \(P=0.003\)), higher preoperative GH (\(b=0.003\), 95% CIs (0.001, 0.004), \(P=0.001\)) and higher prevalence of preoperative hypopituitarism (\(b=0.275\), 95% CIs (0.023, 0.527), \(P=0.033\)) (Supplementary Table 5). Inclusion of the preoperative IGF1 and the weight of the patient contributed to the model strength, although their model coefficients were not significant. This regression model explained 47% of the variance in the extent of treatments.

Low hormonal remission status at the last follow-up associated with poor IGF1 response three months after surgery, controlled for extent of treatments and sex (three-month ∆IGF1 change from ∆IGF1=0 to ∆IGF1=2,
**Table 2** Clinical characteristics of patients with sporadic somatotroph adenomas according to AIP expression status. *AIP* mutation-positive tumors are excluded from analysis.

<table>
<thead>
<tr>
<th>Demographics</th>
<th>Total (n)</th>
<th>Low AIP expression (0–3)</th>
<th>High AIP expression (&gt;3)</th>
<th>r</th>
<th>P</th>
<th>q</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gender, M/F</td>
<td>56</td>
<td>07/05/16</td>
<td>19/25</td>
<td>0.049</td>
<td>0.76</td>
<td>0.97</td>
</tr>
<tr>
<td>Mean age at diagnosis (years)</td>
<td>56</td>
<td>48.5</td>
<td>50.6</td>
<td>0.11</td>
<td>0.44</td>
<td>0.89</td>
</tr>
<tr>
<td>Mean follow-up time (years)*</td>
<td>54</td>
<td>7.8</td>
<td>7.4</td>
<td>0.048</td>
<td>0.74</td>
<td>0.96</td>
</tr>
<tr>
<td>Tumor characteristics</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Macroadenoma, n (%)</td>
<td>56</td>
<td>12 (100)</td>
<td>37 (84.1)</td>
<td>0.2</td>
<td>0.33</td>
<td>0.86</td>
</tr>
<tr>
<td>KNOSP grade 2 or above, n (%)</td>
<td>54</td>
<td>3 (25.0)</td>
<td>9 (20.5)</td>
<td>0.035</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Mean Ki-67</td>
<td>54</td>
<td>2.1</td>
<td>1.4</td>
<td>0.2</td>
<td>0.14</td>
<td>0.62</td>
</tr>
<tr>
<td>Somatic GNAS mutation, n (%)</td>
<td>56</td>
<td>5 (41.7)</td>
<td>16 (36.4)</td>
<td>0.045</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Ga_{2} protein level ≤3, n (%)</td>
<td>56</td>
<td>10 (83.3)</td>
<td>5 (11.4)</td>
<td>0.66</td>
<td>4.51 × 10^{-6}***</td>
<td>9.02 × 10^{-5}***</td>
</tr>
<tr>
<td>Biochemical measurements</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean GH at diagnosis (µg/L)</td>
<td>56</td>
<td>68.5</td>
<td>67.9</td>
<td>0.044</td>
<td>0.75</td>
<td>0.97</td>
</tr>
<tr>
<td>Mean IGF1 at diagnosis, ×ULN</td>
<td>53</td>
<td>2.2</td>
<td>2.3</td>
<td>0.042</td>
<td>0.77</td>
<td>0.97</td>
</tr>
<tr>
<td>Hypopituitarism at diagnosis, n (%)</td>
<td>56</td>
<td>5 (41.7)</td>
<td>19 (43.2)</td>
<td>0.012</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Mean 3-month postoperative GH (µg/L)</td>
<td>54</td>
<td>15</td>
<td>7.6</td>
<td>0.24</td>
<td>0.076</td>
<td>0.4</td>
</tr>
<tr>
<td>Mean 3-month postoperative IGF1 (%ULN/100)</td>
<td>52</td>
<td>0.95</td>
<td>0.79</td>
<td>0.14</td>
<td>0.31</td>
<td>0.86</td>
</tr>
<tr>
<td>In remission at last follow-up visit (%)</td>
<td>56</td>
<td>75</td>
<td>88.1</td>
<td>0.15</td>
<td>0.36</td>
<td>0.87</td>
</tr>
<tr>
<td>Treatment</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Any kind of adjuvant treatment, n (%)</td>
<td>53</td>
<td>5 (41.7)</td>
<td>12 (27.3)</td>
<td>0.11</td>
<td>0.49</td>
<td>0.88</td>
</tr>
<tr>
<td>Radiotherapy, n (%)</td>
<td>53</td>
<td>0 (0)</td>
<td>5 (11.4)</td>
<td>0.16</td>
<td>0.35</td>
<td>0.87</td>
</tr>
<tr>
<td>Mean number of operations, n</td>
<td>56</td>
<td>1.2</td>
<td>1.1</td>
<td>0.14</td>
<td>0.57</td>
<td>0.91</td>
</tr>
<tr>
<td>Somatostatin analogue, n (%)</td>
<td>52</td>
<td>4 (33.3)</td>
<td>12 (27.3)</td>
<td>0.03</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Cabergoline, n (%)</td>
<td>52</td>
<td>3 (25.0)</td>
<td>4 (9.1)</td>
<td>0.18</td>
<td>0.33</td>
<td>0.86</td>
</tr>
<tr>
<td>Pegvisomant, n (%)</td>
<td>52</td>
<td>0 (0)</td>
<td>3 (6.8)</td>
<td>0.13</td>
<td>0.58</td>
<td>0.91</td>
</tr>
</tbody>
</table>

Comparison by Mann–Whitney U test. Statistically significant values are displayed in bold. ***P < 0.001. *Time between diagnostic MRI and last clinical follow-up visit.

$r$, effect size; $P$, $P$ value; $q$, FDR-corrected $P$ value.

\[ b = -0.776, \quad 95\% \text{ CI} \ (-1.032, -0.520), \quad P = 2.07 \times 10^{-7} \] (Supplementary Table 6). A total of 65% of variance in the remission status was explained by the model.

A better IGF1 response at the last follow-up associated with less extensive treatments \((b = 0.418, \quad 95\% \text{ CI} (0.132, 0.705), \quad P = 0.005)\), lower preoperative prolactin level \((b = 1.19 \times 10^{-5}, \quad 95\% \text{ CI} (5.36 \times 10^{-7}, 3.78 \times 10^{-5}), \quad P = 0.044)\) and slightly smaller preoperative GH concentration \((b = -0.003, \quad 95\% \text{ CI} (-0.005, -0.001), \quad P = 0.014)\) (Supplementary Table 7). This model explained only 21% of the total variance in IGF1 response.

**Gsp mutation status and clinical characteristics**

Gain-of-function *GNAS* mutation (*Gsp+*) was observed in 21/59 (35.6%) of the tumors. Association of *Gsp* mutation status to a number of clinical variables was tested using the Mann–Whitney *U* test. *Gsp* status had no effect on AIP or Ga_{2} protein levels *(AIP \(P = 1.0; \quad \text{Ga}_{2} P = 1.0; \quad \text{Supplementary Table 8})*). *Gsp+* tumors showed a nominal association with non-invasive characteristics (KNOSP (grades 0–2), \(P = 0.02, \quad q = 0.121\)), as well as higher preoperative prolactin levels \((P = 0.02, \quad q = 0.119, \quad \text{median} \ 203.0 \text{ng/mL} \quad (\text{Gsp−})\) and 528.0 ng/mL \((\text{Gsp+})\)). However, after correcting for

\[ n = 52, \quad \text{degrees of freedom} \ df = 48, \quad \text{adjusted} \ R^{2} = 0.55, \quad F = 21.4, \quad \text{BIC} = 26.1, \quad P = 6.03 \times 10^{-3} \times \text{***}, \quad b = \text{coefficient}, \text{SE} = \text{standard error}, \quad t = \text{statistic}, \quad P = \text{P-value}, \quad \text{CI} = 95\% \text{ confidence intervals}. \] The constant term $b_0$ of the regression model $y = b_0 + \sum b_i x_i + \epsilon$ denoted by (Constant).

\[ *P < 0.05 \quad \text{and} \quad *** P < 0.001.\]
Table 4  Linear regression model of Ga\(_i\)-2 protein expression level.

<table>
<thead>
<tr>
<th>Variable</th>
<th>(b)</th>
<th>SE</th>
<th>(t)</th>
<th>(P)</th>
<th>CI lower</th>
<th>CI upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>0.08</td>
<td>0.12</td>
<td>0.68</td>
<td>0.50</td>
<td>−0.16</td>
<td>0.33</td>
</tr>
<tr>
<td>AIP</td>
<td>0.78</td>
<td>0.11</td>
<td>7.32</td>
<td>(2.32 \times 10^{-9}***)</td>
<td>0.57</td>
<td>0.99</td>
</tr>
<tr>
<td>Three-month GH</td>
<td>0.0003</td>
<td>0.003</td>
<td>0.10</td>
<td>0.92</td>
<td>−0.10</td>
<td>0.01</td>
</tr>
<tr>
<td>Ki-67</td>
<td>0.04</td>
<td>0.034</td>
<td>1.31</td>
<td>0.20</td>
<td>−0.02</td>
<td>0.11</td>
</tr>
</tbody>
</table>

\(n=52\), degrees of freedom \(df=48\), adjusted \(R^2=0.51\), \(F=18.6\), BIC=33.3, \(P=3.72 \times 10^{-5}***\), \(b\)=coefficient, SE=standard error, \(t=t\) statistic, \(P=P\)-value, CI=95% confidence intervals. The constant term \(b_0\) of the regression model \(y=b_0 + \sum b_i x_i + \epsilon\) denoted by (Constant).

**P<0.001.** Statistically significant values are displayed in bold.

Discussion

We and others have previously reported that AIP germline mutations predispose to pituitary adenomas, mostly to somatotropinomas with an aggressive disease phenotype and a poor response to SSA treatment (5, 7, 15, 22). These recent data suggest that AIP is closely involved in SSA signaling and directly correlates with the therapeutic responses in the patients. In sporadic AIPmut−somatotropinomas, preoperative SSA treatment increases AIP protein expression and the AIP protein levels seem to predict the treatment responses to SSA therapy (12, 14, 21, 23). Recently, we demonstrated that AIP mutations predispose to pituitary tumorigenesis through defective inhibitory GTP-binding protein (Gai) signaling and that Ga\(_i\)-2 protein levels were selectively reduced in AIP-mutated somatotropinomas (9).

Based on these findings, we wanted to examine the possible association between somatotropinoma AIP and Ga\(_i\)-2 protein levels in patients with sporadic acromegaly, a majority of whom (93%) did not receive preoperative SSA treatment, and clinical, biochemical and imaging characteristics of the patients in our cohort of patients operated on at HUH during years 2000–2010 (16, 17). We found AIP and Ga\(_i\)-2 protein expression levels to be strongly associated. Low AIP levels were seen together with reduced Ga\(_i\)-2 protein expression, supporting the earlier finding where reduced Ga\(_i\)-2 levels were detected in AIP-associated somatotropinomas (9). As downregulation of AIP is associated with reduced responsiveness to SSA treatment, and Ga\(_i\) proteins mediate somatostatin signaling via SSTRs (10, 11, 12, 14, 21), the simultaneous downregulation of AIP and Ga\(_i\)-2 may reflect a joint regulation of these proteins on SSA signaling.

Albeit the majority of the AIP protein level variance was explained by Ga\(_i\)-2, also higher proliferative activity (Ki-67) and three-month postoperative GH concentrations

Table 5  Comparison between patients treated by primary surgery only and patients receiving multimodal treatments.

<table>
<thead>
<tr>
<th></th>
<th>Total (n)</th>
<th>Primary surgery only</th>
<th>Primary surgery + any other treatment modality</th>
<th>(r)</th>
<th>(P)</th>
<th>(Q)</th>
</tr>
</thead>
<tbody>
<tr>
<td>F/M</td>
<td>53</td>
<td>18/18</td>
<td>9/8</td>
<td>0.03</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Mean age at diagnosis (years)</td>
<td>53</td>
<td>51.4</td>
<td>47.8</td>
<td>0.11</td>
<td>0.43</td>
<td>0.89</td>
</tr>
<tr>
<td>Mean preoperative GH (µg/L)</td>
<td>53</td>
<td>42.7</td>
<td>129.8</td>
<td>0.54</td>
<td>3.76×10^{-5}***</td>
<td>5.63×10^{-4}***</td>
</tr>
<tr>
<td>Preoperative IGF1 (%ULN/100)</td>
<td>50</td>
<td>2.1</td>
<td>2.4</td>
<td>0.12</td>
<td>0.40</td>
<td>0.89</td>
</tr>
<tr>
<td>Size (micro/macro)</td>
<td>53</td>
<td>5/31</td>
<td>2/15</td>
<td>0.029</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>KNOSP grade &gt;2, n (%)</td>
<td>53</td>
<td>4 (11.1)</td>
<td>8 (47.1)</td>
<td>0.40</td>
<td>0.06**</td>
<td>0.045*</td>
</tr>
<tr>
<td>Somatic GNAS mutation, n (%)</td>
<td>53</td>
<td>16 (44.4)</td>
<td>4 (23.5)</td>
<td>0.20</td>
<td>0.225</td>
<td>0.83</td>
</tr>
<tr>
<td>Ga(_i)-2 protein level ≤3, n (%)</td>
<td>53</td>
<td>10 (27.8)</td>
<td>5 (29.4)</td>
<td>0.017</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>AIP protein level ≤3, n (%)</td>
<td>53</td>
<td>7 (19.4)</td>
<td>5 (29.4)</td>
<td>0.11</td>
<td>0.49</td>
<td>0.89</td>
</tr>
<tr>
<td>Mean Ki-67 proliferation index</td>
<td>51</td>
<td>1.6</td>
<td>1.6</td>
<td>0.029</td>
<td>0.84</td>
<td>1</td>
</tr>
<tr>
<td>Mean 3-month postoperative GH (µg/L)</td>
<td>51</td>
<td>3.4</td>
<td>22.3</td>
<td>0.63</td>
<td>7.53×10^{-7}***</td>
<td>3.01×10^{-5}***</td>
</tr>
<tr>
<td>Mean 3-month postoperative IGF1 (%ULN/100)</td>
<td>50</td>
<td>0.54</td>
<td>1.44</td>
<td>0.59</td>
<td>7.28×10^{-6}***</td>
<td>1.25×10^{-4}***</td>
</tr>
<tr>
<td>In remission at last follow-up visit (%)</td>
<td>52</td>
<td>97.1</td>
<td>64.7</td>
<td>0.44</td>
<td>0.003**</td>
<td>0.031*</td>
</tr>
<tr>
<td>Mean follow-up time (years)</td>
<td>52</td>
<td>7.1</td>
<td>8.8</td>
<td>0.28</td>
<td>0.044*</td>
<td>0.23</td>
</tr>
</tbody>
</table>

Comparison by Mann–Whitney \(U\) test. Statistically significant values are displayed in bold.

\(*P<0.05\), \(**P<0.01\) and ***\(P<0.001\).

\(r\), effect size \((Z/sqrt(N))\), where \(Z\) is the \(Z\) score corresponding to the \(U\) statistic and \(N\) is the total number of samples; \(P\), Mann–Whitney \(U\) test \(P\) value; \(Q\), FDR-corrected \(P\) value.
associated with reduced AIP protein expression. This supports earlier findings that AIPmut− somatotropinomas with reduced AIP levels share characteristics with AIPmut+ tumors. It was demonstrated that AIP downregulation is accompanied by higher proliferative activity and that AIP mutation-associated patients tend to have less effective reduction of GH and IGF1 levels, indicating poorer response to SSA treatments (14, 20, 22). In addition, it has been reported that low AIP level is a good marker of invasiveness in somatotropinomas (14, 21, 23). In the present study, however, no association between invasive features and AIP levels was detected. The reason for this difference might be the fact that in our tumor set, the total number of tumors having aggressive features was low (Table 1). However, low tumor AIP protein levels were significantly associated with higher GH concentrations at last follow-up, which occurred at a mean 7.7 years after surgery (q = 0.045). This is, to the best of our knowledge, the first cohort study on sporadic acromegaly evaluating the possible influence of AIP protein levels of the primary tumors on long-term hormonal outcome, demonstrating that low AIP protein levels predict high GH concentrations even when more than 7 years after primary treatment have elapsed. In addition, regression modeling indicated that the extent of given treatments was best explained by the preoperative GH concentration (P = 7.94 × 10⁻⁴), KNOSP (P = 0.003) and preoperative hypopituitarism (P = 0.03). Remission at the last follow-up was best explained by the change in 3-month postoperative IGF1 (P = 2.07 × 10⁻²). Both low AIP protein level of the primary tumor, a small reduction only in IGF1 concentration 3 months after surgery, as well as preoperative GH, KNOSP grade and preoperative hypopituitarism thus seem to represent early and useful indicators of poor long-term hormonal remission and treatment resistance in sporadic acromegaly.

The current and previous studies suggest that downregulation of AIP protein contributes to the pathogenesis of a subset of AIPmut− somatotropinomas (12, 13, 14, 15, 21, 23). Currently, the mechanisms involved in the reduced AIP levels in these tumors are not known. Low somatic single-nucleotide and structural variant DNA damage rates in pituitary adenomas (2, 3) indicate the involvement of other mechanisms. It has been suggested that alterations in epigenetic regulation may play a prominent role in pituitary neoplasia, likely via loss or reduced expression of tumor suppressor genes (24). Also numerical chromosomal abnormality, aneuploidy and characterize these tumors (3, 25). Hence, these mechanisms may be promising candidates in explaining reduced expression of AIP in these more aggressive AIPmut− somatotropinomas.

Although it has been proposed that Gsp+ associated tumors are more often microadenomas, lacking invasive features, and that patients with Gsp+ associated tumor respond better to SSA treatment, larger studies have shown that there is no difference in clinical features and outcome of patients with or without Gsp mutation (26, 27, 28). Consistent with this, we did not observe any correlation between adenomas with or without Gsp mutation and clinical characteristics. Further, our results agree with the study of Jaffrain-Rea et al. (14) in that no effect on AIP staining intensities was observed between Gsp genotypes. Although inhibitory Ga_i signaling counteracts the stimulatory action of GNAS (Ga_i) in cAMP synthesis, no correlation between Gsp+ genotype and Ga_i2 protein levels was detected.

Although AIP IHC is an important application in research use, the value of IHC for the detection of AIP germline mutation is more challenging. Many of AIP alterations are characterized by an exchange of single amino acid or in-frame insertion/deletion (indels) (5). In such cases, AIP IHC may lead to positive immunostaining, regardless of AIP-associated background of the tumor. Therefore, standard germline sequencing methods should be used for the identification of AIP germline mutations. For instance, multiplex ligation-dependent probe amplification (MLPA) and whole-genome sequencing (WGS) are methods of choice for identification of larger AIP germline indels.

In genetically heterogeneous populations, the prevalence of AIP mutations is generally less than 4% (20, 29, 30, 31, 32). In a Finnish setting, previous AIP mutation frequency studies have focused on a defined, homogenous population from Northern Finland or patients with early-onset disease (7, 29, 33). In the original study of Vierimaa et al. (7) AIP mutations accounted for 16% of population-based acromegaly patients from Northern Finland. In the current study, we examined the prevalence of AIP mutations in a cohort of 60 consecutive patients with sporadic acromegaly, operated at the HUH during 2000–2010, representative of the population in Southern Finland. Normal DNA samples were not available from the patients to perform germline AIP analysis. However, the appearance of a Finnish founder mutation, Q14X, supports the germline origin of this mutation. The AIP mutation prevalence of 6.7% seen in this apparently sporadic somatotropinoma setting is markedly higher than those reported in several prospective international cohort studies (5, 30, 31, 32).
This reflects the genetically homogenous structure of the Finnish population (34), where a Finnish AIP founder mutation (Q14X) accounts for the majority of the pathogenic variants (5, 7, 29, 33). In Finnish patients, we have so far identified altogether 29 Q14X mutations (21 familial and 8 apparently sporadic cases) and in addition, in patients with sporadic acromegaly, we have detected one splice-site mutation (IVS3-1G>A) (7) and two patients with short deletions: c.733>G 735delGAG (9) and c.70>G c.70>GAGCTCCGGACTTTCAAGA (present study). The rareness of these variants compared to the Q14X mutation indicates that they represent more recent events in the Finnish population.

In summary, we have now for the first time shown that in sporadic somatotropinomas, AIP protein expression levels associate with Ga\(_{\alpha_2}\) protein intensities, possibly indicating a synergetic effect of these proteins on SSA signaling. In addition, higher proliferation activity and postroperative GH levels were seen together with reduced AIP protein levels, indicating a more aggressive nature of the tumors and worse treatment response. Both low AIP protein level of the primary tumor as well as a small reduction only in IGFI concentration 3 months after surgery seem to serve as early and useful predictors of treatment resistance and poor long-term hormonal remission in sporadic acromegaly. In addition, the AIP mutation rate of 6.8% in our Finnish population-based series of somatotropinomas is higher than that seen in many other international cohort studies, likely reflecting the special genetic composition of the Finnish population.

Supplementary data
This is linked to the online version of the paper at http://dx.doi.org/10.1530/EJE-16-0620.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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Clinical Study


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